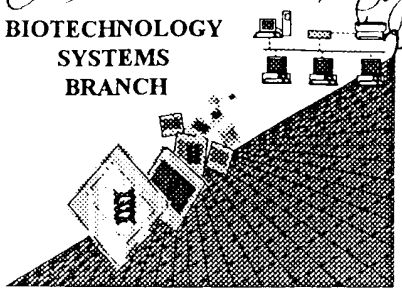
0500 #6

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/492,709

Art Unit / Team No. : OIPE

Date Processed by STIC: 2/15/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

1 <110> Zyskind, Judith
2 Ohlsen, Kari L.
3 Trawick, John
4 Forsyth, R. Allyn
5 Froelich, Jamie M.
6 Carr, Grant J.
7 Yamamoto, Robert T.
8 Xu, H. Howard
9 <120> GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
10 ESCHERICHIA COLI
11 <130> ELITRA.001A
12 <140> US/09/492,709
13 <141> 2000-01-27
E--> CK 14 **<160> 485**
15 <170> FastSEQ for Windows Version 3.0

ERRORED SEQUENCES FOLLOW

E--> 16 **<210> 144**
17 <211> 1197 see p. 6
18 <212> DNA
19 <213> E. Coli
20 <400> 144

21	atgcaggtgg ctgaacagcg cattcagcta gctgaagccc aggcgaaggc agttgccact	60
22	caggatggtc cgcagatcga cttttcggcg gatatggagc ggcaaaaaat gtcggcagaa	120
23	ggcttaatgg ggccgtttgc tctgaacgat ccggccgcag gtacgaccgg cccgtggtac	180
24	accaacggta cttttggctt aacggcgggc tggcatctcg atatctgggg aaagaatcgg	240
25	gcggaggtta ctgcccgcct gggtacggtt aaagcacggg cggcggaacg cgagcaaacc	300
26	cgccaattgc tggctggcag cgtagcccgc ctgtactggg agtggcaaac ccaggcggcg	360
27	ttaaacacgg tcttgcagca aatagaaaaa gagcagaaca ccattatcgc gaccgatcgc	420
28	cagctatatc agaacgggat tacttcttca gttgaaggtg tggaaaccga tattaatgcc	480
29	agcaaaaccc ggcagcagct caacgatgtc gcggggaaaa tgaaaattat tgaggcacgg	540
30	ttaagcgcac ttacaaataa ccagacaaag tcattgaagc ttaaaccggt cgcgttgccg	600
31	aaagtggcaa gccagcttcc tgatgaactg gggtactcct tactggcccg gcgggcagat	660
32	ttgcaggcgg cgcactggta cgttgagtca tcgctaagca ccattgatgc ggcaaaagcg	720
33	gcatttatc ctgacatcaa cctgatggcc ttcctgcaac aggatgcgtt gcacttaagc	780
34	gatctgttcc gtcattccgc gcagcaaatg ggcgttacgg caggcctgac gctacccatt	840
35	ttcgatagtg gtcgtcttaa cgccaatctc gatatcgcaa aagccgaaag caacttgtct	900
36	atcgccagct acaacaaagc ggtggttgaa gcggtgaatg acgtggcgcg ggcagccagt	960
37	caggttcaga cactggcgga gaaaaaccag catcaggcgc aaattgagcg cgatgccttg	1020
38	cgtgtggtag gtcttgcgca ggcgcgcttt aacgcgggca tcattgctgg ttcccgcgtc	1080
39	agcgaagcca gaatccccgc gctgcgtgag cgggccaatg gcctgttatt gcaagggcag	1140

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       40        tggctggatg cctccattca actcactggt gcgttgggcg gggggtacaa acgctga       1197

E-->   41  <210> 309
       42  <211> 173
       43  <212> PRT
       44  <213> E. Coli
       45  <400> 309
       46        Met Ser Lys Pro Lys Tyr Pro Phe Glu Lys Arg Leu Glu Val Val Asn
       47         1               5                  10                  15
       48        His Tyr Phe Thr Thr Asp Asp Gly Tyr Arg Ile Ile Ser Ala Arg Phe
       49                    20                  25                  30
       50        Gly Val Pro Arg Thr Gln Val Arg Thr Trp Val Ala Leu Tyr Glu Lys
       51                35                  40                  45
       52        His Gly Glu Lys Gly Leu Ile Pro Lys Pro Lys Gly Val Ser Ala Asp
       53            50                  55                  60
       54        Pro Glu Leu Arg Ile Lys Val Val Lys Ala Val Ile Glu Gln His Met
       55        65                  70                  75                  80
       56        Ser Leu Asn Gln Ala Ala Ala His Phe Met Leu Ala Gly Ser Gly Ser
       57                        85                  90                  95
       58        Val Ala Arg Trp Leu Lys Val Tyr Glu Glu Arg Gly Glu Ala Gly Leu
       59                    100                 105                 110
       60        Arg Ala Leu Lys Ile Gly Thr Lys Arg Asn Ile Ala Ile Ser Val Asp
       61                115                 120                 125
       62        Pro Glu Lys Ala Ala Ser Ala Leu Glu Leu Ser Lys Asp Arg Arg Ile
       63            130                 135                 140
       64        Glu Asp Leu Glu Arg Gln Val Arg Phe Leu Glu Thr Arg Leu Met Tyr
       65        145                 150                 155                 160
       66        Leu Lys Lys Leu Lys Ala Leu Ala His Pro Thr Lys Lys
       67                        165                 170

       68  <210> 358
E-->   69  <211> 83
       70  <212> RNA
       71  <213> E. Coli
       72  <400> 358
       73        ggugaggugg ccgagaggcu gaaggcgcuc cccugcuaag ggaguaugcg gucaaaagcu      60
E-->   74        gcauccgggg uucgaauccc cgccucaccg cca                                   83

       75  <210> 359
       76  <211> 200
       77  <212> PRT
       78  <213> E. Coli
       79  <400> 359
E-->   80        Met Lys Asn Lys Ala Asp Asn Lys Lys Arg Asn Phe Leu Thr His Ser
       81         1               5                  10                  15
       82        Glu Ile Glu Ser Leu Leu Lys Ala Ala Asn Thr Gly Pro His Ala Ala
       83                    20                  25                  30
       84        Arg Asn Tyr Cys Leu Thr Leu Leu Cys Phe Ile His Gly Phe Arg Ala
       85                35                  40                  45
       86        Ser Glu Ile Cys Arg Leu Arg Ile Ser Asp Ile Asp Leu Lys Ala Lys
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 87              50                  55                  60
 88  Cys Ile Tyr Ile His Arg Leu Lys Lys Gly Phe Ser Thr Thr His Pro
 89  65                  70                  75                  80
 90  Leu Leu Asn Lys Glu Val Gln Ala Leu Lys Asn Trp Leu Ser Ile Arg
 91                  85                  90                  95
 92  Thr Ser Tyr Pro His Ala Glu Ser Glu Trp Val Phe Leu Ser Arg Lys
 93              100                 105                 110
 94  Gly Asn Pro Leu Ser Arg Gln Gln Phe Tyr His Ile Ile Ser Thr Ser
 95          115                 120                 125
 96  Gly Gly Asn Ala Gly Leu Ser Leu Glu Ile His Pro His Met Leu Arg
 97      130                 135                 140
 98  His Ser Cys Gly Phe Ala Leu Ala Asn Met Gly Ile Asp Thr Arg Leu
 99  145                 150                 155                 160
100  Ile Gln Asp Tyr Leu Gly His Arg Asn Ile Arg His Thr Val Trp Tyr
101                  165                 170                 175
102  Thr Ala Ser Asn Ala Gly Arg Phe Tyr Gly Ile Trp Asp Arg Ala Arg
103              180                 185                 190
104  Gly Arg Gln Arg His Ala Val Leu
105          195                 200
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106  <210> 399
E--> 107  <211> 2894   2904 shown (p. 4)
108  <212> RNA
109  <213> E. Coli
110  <400> 399
111  aagguuaagc cucacgguuc auuaguaccg guuagcucaa cgcaucgcug cgcuuacaca      60
112  cccggccuau caacgucguc gucuucaacg uuccuucagg acccuuaaag ggucagggag     120
113  aacucaucuc ggggcaaguu ucgugcuuag augcuuucag cacuuaucuc uuccgcauuu     180
114  agcuaccggg cagugccauu ggcaugacaa cccgaacacc agugaugcgu ccacuccggu     240
115  ccucucguac uaggagcagc cccccucagu ucuccagcgc ccacggcaga uagggaccga     300
116  acugucucac gacguucuaa acccagcucg cguaccacuu uaaauggcga acagccauac     360
117  ccuugggacc uacuucagcc ccaggaugug augagccgac aucgaggugc caaacaccgc     420
118  cgucgauaug aacucuuggg cgguaucagc cuguuauccc cggaguaccu uuuauccguu     480
119  gagcgauggc ccuuccauuc agaaccaccg gaucacuaug accugcuuuc gcaccugcuc     540
120  gcgccgucac gcucgcaguc aagcuggcuu augccauugc acuaaccucc ugauguccga     600
121  ccaggauuag ccaaccuucg ugcuccuccg uuacucuuua ggaggagacc gccccaguca     660
122  aacuacccac cagacacugu ccgcaacccg gauuacgggu caacguuaga acaucaaaca     720
123  uuaaagggug guauuucaag gucggcucca ugcagacugg cguccacacu ucaaagccuc     780
124  ccaccuaucc uacacaucaa ggcucaaugu ucagugucaa gcuauaguaa agguucacgg     840
125  ggucuuuccg ucuugccgcg gguacacugc aucuucacag cgaguucaau uucacugagu     900
126  cucgggugga gacagccugg ccaucauuac gccauucgug caggucggaa cuuacccgac     960
127  aaggaauuuc gcuaccuuag gaccguuaua guuacggccg ccguuuaccg gggcuucgau    1020
128  caagagcuuc gcuugcgcua accccaucaa uuaaccuucc ggcaccgggc aggcgucaca    1080
129  ccguauacgu ccacuuucgu guuugcacag ugcuguguuu uuaauaaaca guugcagcca    1140
130  gcugguaucu ucgacugauu ucagcuccau ccgcgaggga ccucaccuac auaucagcgu    1200
131  gccuucuccc gaaguuacgg caccauuuug ccuaguuccu ucacccgagu ucucucaagc    1260
132  gccuugguau ucucuaccug accaccugug ucgguuuggg guacgauuug auguuaccug    1320
133  augcuuagag gcuuuuccug gaagcagggc auuuguugcu ucagcaccgu agugccucgu    1380
134  caucacgccu cagccuugau uuuccggauu ugccuggaaa accagccuac acgcuuaaac    1440
135  cgggacaacc gucgcccggc caacauagcc uucuccgucc ccccuucgca guaacaccaa    1500
```

	136	guacaggaau auuaaccugu uucccaucga cuacgccuuu cggccucgcc uuaggggucg	1560
	137	acucacccug ccccgauuaa cguuggacag gaacccuugg ucuuccggcg agcgggcuuu	1620
	138	ucacccgcuu uaucguuacu uaugucagca uucgcacuuc ugauaccucc agcaugccuc	1680
	139	acagcacacc uucgcaggcu uacagaacgc uccccuaccc aacaacgcau aagcgucgcu	1740
	140	gccgcagcuu cggugcaugg uuuagccccg uuacaucuuc cgcgcaggcc gacucgacca	1800
	141	gugagcuauu acgcuuucuu uaaaugaugg cugcuucuaa gccaacaucc uggcugucug	1860
	142	ggccuuccca caucguuucc cacuuaacca ugacuuuggg accuuagcug gcggucuggg	1920
	143	uuguuucccu cuucacgacg gacguuagca cccgccgugu gucucccgug auaacauucu	1980
	144	ccgguauucg caguuugcau cggguuggua agucgggaug acccccuugc cgaaacagug	2040
	145	cucuaccccc ggagaugaau ucacgaggcg cuaccuaaau agcuuucggg gagaaccagc	2100
	146	uaucucccgg uuugauuggc cuuucacccc cagccacaag ucauccgcua auuuuucaac	2160
	147	auuagucggu ucgguccucc aguuaguguu acccaaccuu caaccugccc auggcuagau	2220
	148	caccggguuu cgggucuaua cccugcaacu uaacgcccag uuaagacucg guuucccuuc	2280
	149	ggcucccCua uucgguuaac cuugcuacag aauauaaguc gcugacccau uauacaaaag	2340
	150	guacgcaguc acacgccuaa gcgugcuccc acugcuugua cguacacggu uucagguucu	2400
	151	uuuucacucc ccucgccggg guucuuuucg ccuuucccuc acgguacugg uucacuaucg	2460
	152	gucagucagg aguauuuagc cuuggaggau ggucccccca uauucagaca ggauaccacg	2520
	153	ugucccgccc uacucaucga gcucacagca ugugcauuuu uguguacggg gcugucaccc	2580
	154	uguaucgcgc gccuuuccag acgcuuccac uaacacacac acugauucag gcucugggcu	2640
	155	gcucccCguu cgcucgccgc uacuggggga aucucgguug auuucuuuuc cucgggguac	2700
	156	uuagauguuu caguuccccc gguucgccuc auuaaccuau ggauucaguu aaugauagug	2760
	157	ugucgaaaca cacuggguuu ccccauucgg aaaucgccgg uuauaacggu ucauaucacc	2820
	158	uuaccgacgc uuaucgcaga uuagcacguc cuucaucgcc ucugacugcc agggcaucca	2880
E-->	159	**ccguguacgc uuagucgcuu aacc**	**2894**

2904

Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

insert a blank line at the end of Seq. 142

move this over

<210> 143
<211> 186
<212> DNA
<213> E. Coli

<400> 143
atgagcaaag gcgcattata tgaatttaac aatccagatc aactgaaaat acctctccct 60
cataaacaca tagcgtcaac attcaatgac ataatgagta aagatgttgg ttatgcatac 120
gtatcattac tctatgcctg tcccttaaaa acccactcat taagactgaa tccattcagc 180
aaatga 186

→ <210> 308
move over <211> 555
<212> PRT
<213> E. Coli

<400> 308
<400> 3 delete
Met Ala Gln Phe Val Tyr Thr Met His Arg Val Gly Lys Val Val Pro

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/492,709**

DATE: 02/15/2000
TIME: 14:05:42

Input Set: **I492709.RAW**

Line	?	Error/Warning	Original Text
14	E	# of Seq. 485 Not Equal Actual 486	<160> 485
16	E	Seq.#s 1 thru 143 missing	<210> 144
41	E	Seq.#s 1 thru 308 missing	<210> 309
69	E	Input 83, Calc# Bases 93 differ	<211> 83
74	E	Number of Bases conflict w/ Running Total	gcauccgggg uucgaauccc cgccucaccg cca
80	E	Wrong Amino Acid Designator	Meu Lys Asn Lys Ala Asp Asn Lys Lys Arg A
107	E	Input 2894, Calc# Bases 2904 differ	<211> 2894
159	E	Number of Bases conflict w/ Running Total	ccguguacgc uuagucgcuu aacc